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GenCore version 4.5

Om protein - protein search, using sw model

Run on: March 1, 2001, 16:09:23 ; Search time 299.73 Seconds
(without alignments)
16.815 Million cell updates/sec

Title: US-09-331-631A-5_COPY_33_75

Perfect score: 248

Sequence: 1 NOEDPOTECOCQRCRQESFDPROOYCORRCREICEEEYY 43

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTRIMBL_15,*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_minc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rodont:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB	ID	Description
1	248	100.0	625	10	Q9SPBL3	Q9SPBL3 macadamia i
2	241	97.2	666	10	Q9SPBL5	Q9SPBL5 macadamia i
3	94.8	666	10	Q9SPBL4	Q9SPBL4 macadamia i	
4	45.2	593	10	Q9SPBW4	Q9SPBW4 juglans reg	
5	110	44.4	525	10	Q93358	Q93358 theobroma c
6	96	38.7	411	5	P91419	P91419 caenorhabdi
7	78.5	31.7	425	5	Q17400	Q17400 caenorhabdi
8	78.5	31.7	600	5	Q17401	Q17401 caenorhabdi
9	77	31.0	572	5	Q19594	Q19594 caenorhabdi
10	77	31.0	1513	5	Q17970	Q17970 caenorhabdi
11	75.5	30.4	242	5	Q19919	Q19919 caenorhabdi
12	75	30.2	388	5	Q16500	Q16500 caenorhabdi
13	75	30.2	388	5	Q16501	Q16501 caenorhabdi
14	75	30.2	388	5	Q14606	Q14606 caenorhabdi
15	74	29.8	438	5	Q16502	Q16502 caenorhabdi
16	74	29.8	445	5	Q16511	Q16511 caenorhabdi
17	73.5	29.6	810	10	Q9ZW13	Q9ZW13 cucurbita m
18	73	29.4	330	5	Q18118	Q18118 caenorhabdi
19	29.4				Q9n4rl	Q9n4rl caenorhabdi

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4	45.2	593	10	Q9SPBW4	Q9SPBW4 juglans reg	
5	110	44.4	525	10	Q93358	Q93358 theobroma c
6	96					

Db 78 EEEIQRQOCOCGRCQEQGOREQQCQRCWEQYRQE 117
 RESULT 6
 ID P91419 PRELIMINARY; PRT; 411 AA.
 AC P91419;
 DT 01-MAY-1997 (TREMBLREL. 03, Created)
 DT 01-MAY-1997 (TREMBLREL. 03, Last sequence update)
 DT 01-NOV-1998 (TREMBLREL. 08, Last annotation update)
 DE CODED FOR BY C. ELEGANS CDNA YK115A6.5.
 GN T01D1.6.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TAXID=6239;
 RN [1]
 SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RX MEDLINE-94150718; PubMed=7906398;
 RA Wilson R., Alnscough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
 RA Jones M., Kershaw J., Kirsten J., Laister N., Latrellie P.,
 RA Lightfoot J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Shownkeen R.,
 RA Smildon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
 RA Thiley-Mieg J., Thomas K., Vaudin M., Vaughan M., Waterston R.,
 RA Watson R., Wainstock L., Wilkinson-Sproat J., Wohldmann P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 elegans";
 RT elegans";
 RL Nature 368:32-38(1994).
 RN [2]
 SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Bradshaw H., Wohldmann P.;
 RL Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Waterston R.;
 DR Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
 EMBL; U80455; AAB37887.1; -
 SEQUENCE 411 AA; 44675 MW; 599DAC9DCFB1382 CRC64;
 RN [1]
 SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA McMurray A.;
 RL Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; Z71177; CAA94683.1; -
 DR WORMPEP; AC3.4; CB05134;
 DR INTERPRO; IPR001594; -
 DR PFAM; PF01529; ZF-DHHC; 1.
 DR PRODOM; PD003041; -; 1.
 DR PRODOM; PD003041; -; 1.
 KW Hypothetical protein: Transmembrane.
 FT TRANSMEM 309 329 POTENTIAL.
 FT TRANSMEM 447 467 POTENTIAL.
 FT TRANSMEM 490 510 POTENTIAL.
 FT DOMAIN 6 287 GLN-RICH.
 SQ SEQUENCE 600 AA; 67740 MW; 504ACCEB1A72091B CRC64;
 RESULT 7
 ID Q17400 PRELIMINARY; PRT; 425 AA.
 AC Q17400;
 DT 01-JAN-1999 (TREMBLREL. 09, Created)
 DT 01-JAN-1999 (TREMBLREL. 09, Last sequence update)
 DT 01-JAN-1999 (TREMBLREL. 09, Last annotation update)
 DE HYPOTHETICAL 45.9 KDA PROTEIN AC3.3 IN CHROMOSOME V PRECURSOR.
 GN AC3.3.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TAXID=6239;
 RN [1]
 SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA McMurray A.;
 RESULT 9
 ID Q19594 PRELIMINARY; PRT; 572 AA.
 AC Q19594;

Query Match 30.2%; Score 75; DB 5; Length 388;
 Best Local Similarity 37.5%; Pred. No. 0.13; Indels 2; Gaps 2;
 Matches 15; Conservative 7; Mismatches 16; Indels 2; Gaps 2;

QY 2 QDPQTEC-0QQRQEQSDPRQ QQYCORRCKEICEE 39
 Db 194 QAQCPQCPQQCQSCVQQQSQSNQEPACNQCSDICQQ 233

RESULT 13
 ID 016501 PRELIMINARY; PRT; 388 AA.
 AC 016501;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE C03A7.7 PROTEIN.
 DE C03A7.7.
 GN Caenorhabditis elegans.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peioderinae; Caenorhabditis.
 OC NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RX MEDLINE=94150718; PubMed=7906398;
 RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
 RA Jones M., Kershaw J., Kistner J., Lalister N., Latreille P.,
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Riffen L., Roopra A., Saunders D., Showkeen R.,
 RA Smalton N., Smith A., Sonnhammer E., Staden R., Sulston J.,
 RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
 RA Watson A., Weinstock L., Wilkinson-Sprott J., Wohldman P.,
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans.";
 RL Nature 368:32-38(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA Sammons L., Wohldman P., Bauer C., Antoniou B., Wilson R.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA Waterston R.;
 RA Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF03046; AAB94214; 1; -.
 SQ SEQUENCE 388 AA; 41440 MW; EA9C34AA4EABFE46 CRC64;

Query Match 30.2%; Score 75; DB 5; Length 388;
 Best Local Similarity 22.2%; Pred. No. 0.13; Indels 14; Gaps 2;
 Matches 15; Conservative 15; Mismatches 12; Indels 22; Gaps 2;

QY 2 QDPQTEC-0QQRQEQSDPRQ QQYCORRCKEICEE 39
 Db 147 QQPASOCOPCQQCNVACIDAPATSTQAPQVWHOLEIQQAQDQCOPCQQCQSQCTQ 206

QY 40 FBE 42
 Db 207 000 209

RESULT 15
 ID 016502 PRELIMINARY; PRT; 438 AA.
 AC 016502;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE C03A7.8 PROTEIN.
 DE C03A7.8.
 GN Caenorhabditis elegans.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peioderinae; Caenorhabditis.
 OC NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=BRISTOL N2;
 RX MEDLINE=94150718; PubMed=7906398;
 RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 RA Croxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
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 RA Smalton N., Smith A., Sonhamer E., Staden R., Sulston J.,
 RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
 RA Watson A., Weinstock L., Wilkinson-Sproat J., Woldman P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans";
 RL Nature 368:32-38(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA Greco T., Bradshaw H., Elliott G.;
 RL Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA Waterston R.;
 RL Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
 DR EMBL: AF016451; AAB65995 1; -;
 SQ SEQUENCE 438 AA; 47502 MW; 835C4F68RCF510B1 CRC64;

Query Match 29.8%; Score 74; DB 5; Length 438;
 Best Local Similarity 30.2%; Pred. No. 0.19;
 Matches 13; Conservative 12; Mismatches 12; Indels 6; Gaps 2;
 OY 3 EDPQTECQ-OCQRG-----RQRESDPQQYCORKECCE 39
 Db 191 QQAQHQCQPCQQQQQQSCVQQQPSITQCBPACWQCSDICQQ 233

Search completed: March 1, 2001, 16:09:23
 Job time: 1567 sec